

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

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(i) APPLICANT: Anderson, Dirk M.  
Galibert, Laurent  
Maraskovsky, Eugene

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(ii) TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

(iii) NUMBER OF SEQUENCES: 19

15

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Immunex Corporation, Law Department  
(B) STREET: 51 University Street  
(C) CITY: Seattle  
(D) STATE: WA  
(E) COUNTRY: USA  
(F) ZIP: 98101

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: Apple Power Macintosh  
(C) OPERATING SYSTEM: Apple Operating System 7.5.5  
(D) SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

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(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE: 22 DECEMBER 1997  
(C) CLASSIFICATION:

30

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: USSN 60/064,671  
(B) FILING DATE: 14 OCTOBER 1997  
(C) CLASSIFICATION:

35

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: USSN 08/813,509  
(B) FILING DATE: 07 MARCH 1997  
(C) CLASSIFICATION:

40

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: USSN 08/772,330 (60/064,671)  
(B) FILING DATE: 23 DECEMBER 1996  
(C) CLASSIFICATION:

45

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Perkins, Patricia Anne  
(B) REGISTRATION NUMBER: 34,693  
(C) REFERENCE/DOCKET NUMBER: 2852-A

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(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (206)587-0430  
(B) TELEFAX: (206)233-0644

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## (2) INFORMATION FOR SEQ ID NO:1:

60

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 3115 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

10

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: HOMO SAPIENS

15

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: BONE-MARROW DERIVED DENDRITIC CELLS

(B) CLONE: 9D-8A

20

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 93..1868

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCTGCTGCTG CTCTGCGCGC TGCTCGCCCG GCTGCAGTTT TATCCAGAAA GAGCTGTGTG 60

GACTCTCTGC CTGACCTCAG TGTTCTTTTC AG GTG GCT TTG CAG ATC GCT CCT 113

30

Val Ala Leu Gln Ile Ala Pro  
 1 5

CCA TGT ACC AGT GAG AAG CAT TAT GAG CAT CTG GGA CGG TGC TGT AAC 161  
 Pro Cys Thr Ser Glu Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn  
 10 15 20

35

AAA TGT GAA CCA GGA AAG TAC ATG TCT TCT AAA TGC ACT ACT ACC TCT 209  
 Lys Cys Glu Pro Gly Lys Tyr Met Ser Ser Lys Cys Thr Thr Thr Ser  
 25 30 35

40

GAC AGT GTA TGT CTG CCC TGT GGC CCG GAT GAA TAC TTG GAT AGC TGG 257  
 Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp  
 40 45 50 55

45

AAT GAA GAA GAT AAA TGC TTG CTG CAT AAA GTT TGT GAT ACA GGC AAG 305  
 Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys  
 60 65 70

50

GCC CTG GTG GCC GTG GTC GCC GGC AAC AGC ACG ACC CCC CGG CGC TGC 353  
 Ala Leu Val Ala Val Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys  
 75 80 85

55

GCG TGC ACG GCT GGG TAC CAC TGG AGC CAG GAC TGC GAG TGC TGC CGC 401  
 Ala Cys Thr Ala Gly Tyr His Trp Ser Gln Asp Cys Glu Cys Cys Arg  
 90 95 100

CGC AAC ACC GAG TGC GCG CCG GGC CTG GGC GCC CAG CAC CCG TTG CAG 449  
 Arg Asn Thr Glu Cys Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln  
 105 110 115

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	CTC	AAC	AAG	GAC	ACA	GTG	TGC	AAA	CCT	TGC	CTT	GCA	GGC	TAC	TTC	TCT	497
	Leu	Asn	Lys	Asp	Thr	Val	Cys	Lys	Pro	Cys	Leu	Ala	Gly	Tyr	Phe	Ser	
	120					125					130					135	
5	GAT	GCC	TTT	TCC	TCC	ACG	GAC	AAA	TGC	AGA	CCC	TGG	ACC	AAC	TGT	ACC	545
	Asp	Ala	Phe	Ser	Ser	Thr	Asp	Lys	Cys	Arg	Pro	Trp	Thr	Asn	Cys	Thr	
					140					145					150		
10	TTC	CTT	GGA	AAG	AGA	GTA	GAA	CAT	CAT	GGG	ACA	GAG	AAA	TCC	GAT	GCG	593
	Phe	Leu	Gly	Lys	Arg	Val	Glu	His	His	Gly	Thr	Glu	Lys	Ser	Asp	Ala	
				155					160					165			
15	GTT	TGC	AGT	TCT	TCT	CTG	CCA	GCT	AGA	AAA	CCA	CCA	AAT	GAA	CCC	CAT	641
	Val	Cys	Ser	Ser	Ser	Leu	Pro	Ala	Arg	Lys	Pro	Pro	Asn	Glu	Pro	His	
			170					175					180				
20	GTT	TAC	TTG	CCC	GGT	TTA	ATA	ATT	CTG	CTT	CTC	TTC	GCG	TCT	GTG	GCC	689
	Val	Tyr	Leu	Pro	Gly	Leu	Ile	Ile	Leu	Leu	Leu	Phe	Ala	Ser	Val	Ala	
		185					190					195					
25	CTG	GTG	GCT	GCC	ATC	ATC	TTT	GGC	GTT	TGC	TAT	AGG	AAA	AAA	GGG	AAA	737
	Leu	Val	Ala	Ala	Ile	Ile	Phe	Gly	Val	Cys	Tyr	Arg	Lys	Lys	Gly	Lys	
	200					205					210					215	
30	GCA	CTC	ACA	GCT	AAT	TTG	TGG	CAC	TGG	ATC	AAT	GAG	GCT	TGT	GGC	CGC	785
	Ala	Leu	Thr	Ala	Asn	Leu	Trp	His	Trp	Ile	Asn	Glu	Ala	Cys	Gly	Arg	
					220					225					230		
35	CTA	AGT	GGA	GAT	AAG	GAG	TCC	TCA	GGT	GAC	AGT	TGT	GTC	AGT	ACA	CAC	833
	Leu	Ser	Gly	Asp	Lys	Glu	Ser	Ser	Gly	Asp	Ser	Cys	Val	Ser	Thr	His	
				235				240					245				
40	ACG	GCA	AAC	TTT	GGT	CAG	CAG	GGA	GCA	TGT	GAA	GGT	GTC	TTA	CTG	CTG	881
	Thr	Ala	Asn	Phe	Gly	Gln	Gln	Gly	Ala	Cys	Glu	Gly	Val	Leu	Leu	Leu	
			250					255					260				
45	ACT	CTG	GAG	GAG	AAG	ACA	TTT	CCA	GAA	GAT	ATG	TGC	TAC	CCA	GAT	CAA	929
	Thr	Leu	Glu	Glu	Lys	Thr	Phe	Pro	Glu	Asp	Met	Cys	Tyr	Pro	Asp	Gln	
		265					270					275					
50	GGT	GGT	GTC	TGT	CAG	GGC	ACG	TGT	GTA	GGA	GGT	GGT	CCC	TAC	GCA	CAA	977
	Gly	Gly	Val	Cys	Gln	Gly	Thr	Cys	Val	Gly	Gly	Gly	Pro	Tyr	Ala	Gln	
	280					285					290					295	
55	GGC	GAA	GAT	GCC	AGG	ATG	CTC	TCA	TTG	GTC	AGC	AAG	ACC	GAG	ATA	GAG	1025
	Gly	Glu	Asp	Ala	Arg	Met	Leu	Ser	Leu	Val	Ser	Lys	Thr	Glu	Ile	Glu	
					300					305					310		
60	GAA	GAC	AGC	TTC	AGA	CAG	ATG	CCC	ACA	GAA	GAT	GAA	TAC	ATG	GAC	AGG	1073
	Glu	Asp	Ser	Phe	Arg	Gln	Met	Pro	Thr	Glu	Asp	Glu	Tyr	Met	Asp	Arg	
				315					320					325			
65	CCC	TCC	CAG	CCC	ACA	GAC	CAG	TTA	CTG	TTC	CTC	ACT	GAG	CCT	GGA	AGC	1121
	Pro	Ser	Gln	Pro	Thr	Asp	Gln	Leu	Leu	Phe	Leu	Thr	Glu	Pro	Gly	Ser	
			330					335					340				
70	AAA	TCC	ACA	CCT	CCT	TTC	TCT	GAA	CCC	CTG	GAG	GTG	GGG	GAG	AAT	GAC	1169
	Lys	Ser	Thr	Pro	Pro	Phe	Ser	Glu	Pro	Leu	Glu	Val	Gly	Glu	Asn	Asp	
		345					350					355					

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	AGT	TTA	AGC	CAG	TGC	TTC	ACG	GGG	ACA	CAG	AGC	ACA	GTG	GGT	TCA	GAA	1217
	Ser	Leu	Ser	Gln	Cys	Phe	Thr	Gly	Thr	Gln	Ser	Thr	Val	Gly	Ser	Glu	
	360					365					370					375	
5	AGC	TGC	AAC	TGC	ACT	GAG	CCC	CTG	TGC	AGG	ACT	GAT	TGG	ACT	CCC	ATG	1265
	Ser	Cys	Asn	Cys	Thr	Glu	Pro	Leu	Cys	Arg	Thr	Asp	Trp	Thr	Pro	Met	
					380					385					390		
10	TCC	TCT	GAA	AAC	TAC	TTG	CAA	AAA	GAG	GTG	GAC	AGT	GGC	CAT	TGC	CCG	1313
	Ser	Ser	Glu	Asn	Tyr	Leu	Gln	Lys	Glu	Val	Asp	Ser	Gly	His	Cys	Pro	
				395					400					405			
15	CAC	TGG	GCA	GCC	AGC	CCC	AGC	CCC	AAC	TGG	GCA	GAT	GTC	TGC	ACA	GGC	1361
	His	Trp	Ala	Ala	Ser	Pro	Ser	Pro	Asn	Trp	Ala	Asp	Val	Cys	Thr	Gly	
			410					415					420				
20	TGC	CGG	AAC	CCT	CCT	GGG	GAG	GAC	TGT	GAA	CCC	CTC	GTG	GGT	TCC	CCA	1409
	Cys	Arg	Asn	Pro	Pro	Gly	Glu	Asp	Cys	Glu	Pro	Leu	Val	Gly	Ser	Pro	
		425				430						435					
25	AAA	CGT	GGA	CCC	TTG	CCC	CAG	TGC	GCC	TAT	GGC	ATG	GGC	CTT	CCC	CCT	1457
	Lys	Arg	Gly	Pro	Leu	Pro	Gln	Cys	Ala	Tyr	Gly	Met	Gly	Leu	Pro	Pro	
	440					445					450					455	
30	GAA	GAA	GAA	GCC	AGC	AGG	ACG	GAG	GCC	AGA	GAC	CAG	CCC	GAG	GAT	GGG	1505
	Glu	Glu	Glu	Ala	Ser	Arg	Thr	Glu	Ala	Arg	Asp	Gln	Pro	Glu	Asp	Gly	
					460					465					470		
35	GCT	GAT	GGG	AGG	CTC	CCA	AGC	TCA	GCG	AGG	GCA	GGT	GCC	GGG	TCT	GGA	1553
	Ala	Asp	Gly	Arg	Leu	Pro	Ser	Ser	Ala	Arg	Ala	Gly	Ala	Gly	Ser	Gly	
				475				480						485			
40	AGC	TCC	CCT	GGT	GGC	CAG	TCC	CCT	GCA	TCT	GGA	AAT	GTG	ACT	GGA	AAC	1601
	Ser	Ser	Pro	Gly	Gly	Gln	Ser	Pro	Ala	Ser	Gly	Asn	Val	Thr	Gly	Asn	
			490					495					500				
45	AGT	AAC	TCC	ACG	TTC	ATC	TCC	AGC	GGG	CAG	GTG	ATG	AAC	TTC	AAG	GGC	1649
	Ser	Asn	Ser	Thr	Phe	Ile	Ser	Ser	Gly	Gln	Val	Met	Asn	Phe	Lys	Gly	
		505					510					515					
50	GAC	ATC	ATC	GTG	GTC	TAC	GTC	AGC	CAG	ACC	TCG	CAG	GAG	GGC	GCG	GCG	1697
	Asp	Ile	Ile	Val	Val	Tyr	Val	Ser	Gln	Thr	Ser	Gln	Glu	Gly	Ala	Ala	
	520					525					530					535	
55	GCG	GCT	GCG	GAG	CCC	ATG	GGC	CGC	CCG	GTG	CAG	GAG	GAG	ACC	CTG	GCG	1745
	Ala	Ala	Ala	Glu	Pro	Met	Gly	Arg	Pro	Val	Gln	Glu	Glu	Thr	Leu	Ala	
					540					545					550		
60	CGC	CGA	GAC	TCC	TTC	GCG	GGG	AAC	GGC	CCG	CGC	TTC	CCG	GAC	CCG	TGC	1793
	Arg	Arg	Asp	Ser	Phe	Ala	Gly	Asn	Gly	Pro	Arg	Phe	Pro	Asp	Pro	Cys	
				555					560					565			
65	GGC	GGC	CCC	GAG	GGG	CTG	CGG	GAG	CCG	GAG	AAG	GCC	TCG	AGG	CCG	GTG	1841
	Gly	Gly	Pro	Glu	Gly	Leu	Arg	Glu	Pro	Glu	Lys	Ala	Ser	Arg	Pro	Val	
			570					575					580				
70	CAG	GAG	CAA	GGC	GGG	GCC	AAG	GCT	TGA	GCG	CCCCCCCCA	TGGCTGGGAG					1888
	Gln	Glu	Gln	Gly	Gly	Ala	Lys	Ala									
		585					590										
75	CCCGAAGCTC	GGAGCCAGGG	CTCGCGAGGG	CAGCACCGCA	GCCTCTGCCC	CAGCCCCGGC											1948

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5 CACCCAGGGA TCGATCGGTA CAGTCGAGGA AGACCACCCG GCATTCTCTG CCCACTTTGC 2008  
 CTTCCAGGAA ATGGGCTTTT CAGGAAGTGA ATTGATGAGG ACTGTCCCCA TGCCCACGGA 2068  
 TGCTCAGCAG CCCGCCGCAC TGGGGCAGAT GTCTCCCCTG CCACTCCTCA AACTCGCAGC 2128  
 AGTAATTTGT GGCACATATGA CAGCTATTTT TATGACTATC CTGTTCTGTG GGGGGGGGGT 2188  
 10 CTATGTTTTTC CCCCATATT TGTATTCCTT TTCATAACTT TTCTTGATAT CTTTCCTCCC 2248  
 TCTTTTTTTAA TGTAAGGTT TTCTCAAAAA TTCTCCTAAA GGTGAGGGTC TCTTTCTTTT 2308  
 CTCTTTTCCT TTTTTTTTTC TTTTTTTTGGC AACCTGGCTC TGGCCCAGGC TAGAGTGCAG 2368  
 15 TGGTGCGATT ATAGCCCGGT GCAGCCTCTA ACTCCTGGGC TCAAGCAATC CAAGTGATCC 2428  
 TCCACCTCA ACCTTCGGAG TAGCTGGGAT CACAGCTGCA GGCCACGCCC AGCTTCCTCC 2488  
 20 CCCCAGCTCC CCCCCCCCAG AGACACGGTC CCACCATGTT ACCCAGCCTG GTCTCAAACCT 2548  
 CCCCAGCTAA AGCAGTCCTC CAGCCTCGGC CTCCCAAAGT ACTGGGATT CAGGCGTGAG 2608  
 25 CCCCCACGCT GGCCTGCTTT ACGTATTTTC TTTTGTGCCC CTGCTCACAG TGTTTATAGAG 2668  
 ATGGCTTTCC CAGTGTGTGT TCATTGTAAA CACTTTTGGG AAAGGGCTAA ACATGTGAGG 2728  
 CCTGGAGATA GTTGCTAAGT TGCTAGGAAC ATGTGGTGGG ACTTTCATAT TCTGAAAAAT 2788  
 30 GTTCTATATT CTCATTTTTC TAAAAGAAAG AAAAAAGGAA ACCCGATTTA TTTCTCCTGA 2848  
 ATCTTTTTTAA GTTTGTGTCG TTCCTTAAGC AGAACTAAGC TCAGTATGTG ACCTTACCCG 2908  
 35 CTAGGTGGTT AATTTATCCA TGCTGGCAGA GGCACCTCAGG TACTTGGTAA GCAAATTTCT 2968  
 AAAACTCCAA GTTGCTGCAG CTTGGCATTC TTCTTATTCT AGAGGTCTCT CTGGAAGAGA 3028  
 TGGAGAAAAT GAACAGGACA TGGGGCTCCT GGAAAGAAAG GGCCCGGGAA GTTCAAGGAA 3088  
 40 GAATAAAGTT GAAATTTTAA AAAAAA 3115

## (2) INFORMATION FOR SEQ ID NO:2:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 591 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

55 Val Ala Leu Gln Ile Ala Pro Pro Cys Thr Ser Glu Lys His Tyr Glu  
 1 5 10 15  
 His Leu Gly Arg Cys Cys Asn Lys Cys Glu Pro Gly Lys Tyr Met Ser  
 20 25 30  
 60 Ser Lys Cys Thr Thr Thr Ser Asp Ser Val Cys Leu Pro Cys Gly Pro  
 35 40 45

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Asp Glu Tyr Leu Asp Ser Trp Asn Glu Glu Asp Lys Cys Leu Leu His  
 50 55 60

5 Lys Val Cys Asp Thr Gly Lys Ala Leu Val Ala Val Val Ala Gly Asn  
 65 70 75 80

Ser Thr Thr Pro Arg Arg Cys Ala Cys Thr Ala Gly Tyr His Trp Ser  
 85 90 95

10 Gln Asp Cys Glu Cys Cys Arg Arg Asn Thr Glu Cys Ala Pro Gly Leu  
 100 105 110

15 Gly Ala Gln His Pro Leu Gln Leu Asn Lys Asp Thr Val Cys Lys Pro  
 115 120 125

Cys Leu Ala Gly Tyr Phe Ser Asp Ala Phe Ser Ser Thr Asp Lys Cys  
 130 135 140

20 Arg Pro Trp Thr Asn Cys Thr Phe Leu Gly Lys Arg Val Glu His His  
 145 150 155 160

Gly Thr Glu Lys Ser Asp Ala Val Cys Ser Ser Ser Leu Pro Ala Arg  
 165 170 175

25 Lys Pro Pro Asn Glu Pro His Val Tyr Leu Pro Gly Leu Ile Ile Leu  
 180 185 190

30 Leu Leu Phe Ala Ser Val Ala Leu Val Ala Ala Ile Ile Phe Gly Val  
 195 200 205

Cys Tyr Arg Lys Lys Gly Lys Ala Leu Thr Ala Asn Leu Trp His Trp  
 210 215 220

35 Ile Asn Glu Ala Cys Gly Arg Leu Ser Gly Asp Lys Glu Ser Ser Gly  
 225 230 235 240

Asp Ser Cys Val Ser Thr His Thr Ala Asn Phe Gly Gln Gln Gly Ala  
 245 250 255

40 Cys Glu Gly Val Leu Leu Leu Thr Leu Glu Glu Lys Thr Phe Pro Glu  
 260 265 270

45 Asp Met Cys Tyr Pro Asp Gln Gly Gly Val Cys Gln Gly Thr Cys Val  
 275 280 285

Gly Gly Gly Pro Tyr Ala Gln Gly Glu Asp Ala Arg Met Leu Ser Leu  
 290 295 300

50 Val Ser Lys Thr Glu Ile Glu Glu Asp Ser Phe Arg Gln Met Pro Thr  
 305 310 315 320

Glu Asp Glu Tyr Met Asp Arg Pro Ser Gln Pro Thr Asp Gln Leu Leu  
 325 330 335

55 Phe Leu Thr Glu Pro Gly Ser Lys Ser Thr Pro Pro Phe Ser Glu Pro  
 340 345 350

60 Leu Glu Val Gly Glu Asn Asp Ser Leu Ser Gln Cys Phe Thr Gly Thr  
 355 360 365

0068450-101300

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Gln Ser Thr Val Gly Ser Glu Ser Cys Asn Cys Thr Glu Pro Leu Cys  
 370 375 380  
 5 Arg Thr Asp Trp Thr Pro Met Ser Ser Glu Asn Tyr Leu Gln Lys Glu  
 385 390 395 400  
 Val Asp Ser Gly His Cys Pro His Trp Ala Ala Ser Pro Ser Pro Asn  
 405 410 415  
 10 Trp Ala Asp Val Cys Thr Gly Cys Arg Asn Pro Pro Gly Glu Asp Cys  
 420 425 430  
 Glu Pro Leu Val Gly Ser Pro Lys Arg Gly Pro Leu Pro Gln Cys Ala  
 435 440 445  
 15 Tyr Gly Met Gly Leu Pro Pro Glu Glu Glu Ala Ser Arg Thr Glu Ala  
 450 455 460  
 20 Arg Asp Gln Pro Glu Asp Gly Ala Asp Gly Arg Leu Pro Ser Ser Ala  
 465 470 475 480  
 Arg Ala Gly Ala Gly Ser Gly Ser Ser Pro Gly Gly Gln Ser Pro Ala  
 485 490 495  
 25 Ser Gly Asn Val Thr Gly Asn Ser Asn Ser Thr Phe Ile Ser Ser Gly  
 500 505 510  
 Gln Val Met Asn Phe Lys Gly Asp Ile Ile Val Val Tyr Val Ser Gln  
 515 520 525  
 30 Thr Ser Gln Glu Gly Ala Ala Ala Ala Glu Pro Met Gly Arg Pro  
 530 535 540  
 Val Gln Glu Glu Thr Leu Ala Arg Arg Asp Ser Phe Ala Gly Asn Gly  
 545 550 555 560  
 Pro Arg Phe Pro Asp Pro Cys Gly Gly Pro Glu Gly Leu Arg Glu Pro  
 565 570 575  
 40 Glu Lys Ala Ser Arg Pro Val Gln Glu Gln Gly Gly Ala Lys Ala  
 580 585 590

## (2) INFORMATION FOR SEQ ID NO:3:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1391 base pairs  
 (B) TYPE: nucleic acid  
 50 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: cDNA  
 55 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 60 (A) ORGANISM: HOMO SAPIENS  
 (vii) IMMEDIATE SOURCE:

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(A) LIBRARY: BONE-MARROW DERIVED DENDRITIC CELLS  
(B) CLONE: 9D-15C

## (ix) FEATURE:

5 (A) NAME/KEY: CDS  
(B) LOCATION: 39..1391

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

10 CCGCTGAGGC CGCGGCGCCC GCCAGCCTGT CCCGCGCC ATG GCC CCG CGC GCC 53  
Met Ala Pro Arg Ala  
1 5

15 CGG CGG CGC CGC CCG CTG TTC GCG CTG CTG CTG CTC TGC GCG CTG CTC 101  
Arg Arg Arg Arg Pro Leu Phe Ala Leu Leu Leu Leu Cys Ala Leu Leu  
10 15 20

20 GCC CGG CTG CAG GTG GCT TTG CAG ATC GCT CCT CCA TGT ACC AGT GAG 149  
Ala Arg Leu Gln Val Ala Leu Gln Ile Ala Pro Pro Cys Thr Ser Glu  
25 30 35

25 AAG CAT TAT GAG CAT CTG GGA CGG TGC TGT AAC AAA TGT GAA CCA GGA 197  
Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn Lys Cys Glu Pro Gly  
40 45 50

30 AAG TAC ATG TCT TCT AAA TGC ACT ACT ACC TCT GAC AGT GTA TGT CTG 245  
Lys Tyr Met Ser Ser Lys Cys Thr Thr Thr Ser Asp Ser Val Cys Leu  
55 60 65

35 CCC TGT GGC CCG GAT GAA TAC TTG GAT AGC TGG AAT GAA GAA GAT AAA 293  
Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp Asn Glu Glu Asp Lys  
70 75 80 85

40 TGC TTG CTG CAT AAA GTT TGT GAT ACA GGC AAG GCC CTG GTG GCC GTG 341  
Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys Ala Leu Val Ala Val  
90 95 100

45 GTC GCC GGC AAC AGC ACG ACC CCC CGG CGC TGC GCG TGC ACG GCT GGG 389  
Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys Ala Cys Thr Ala Gly  
105 110 115

50 TAC CAC TGG AGC CAG GAC TGC GAG TGC TGC CGC CGC AAC ACC GAG TGC 437  
Tyr His Trp Ser Gln Asp Cys Glu Cys Cys Arg Arg Asn Thr Glu Cys  
120 125 130

55 GCG CCG GGC CTG GGC GCC CAG CAC CCG TTG CAG CTC AAC AAG GAC ACA 485  
Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln Leu Asn Lys Asp Thr  
135 140 145

60 GTG TGC AAA CCT TGC CTT GCA GGC TAC TTC TCT GAT GCC TTT TCC TCC 533  
Val Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser Asp Ala Phe Ser Ser  
150 155 160 165

55 ACG GAC AAA TGC AGA CCC TGG ACC AAC TGT ACC TTC CTT GGA AAG AGA 581  
Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr Phe Leu Gly Lys Arg  
170 175 180

60 GTA GAA CAT CAT GGG ACA GAG AAA TCC GAT GCG GTT TGC AGT TCT TCT 629  
Val Glu His His Gly Thr Glu Lys Ser Asp Ala Val Cys Ser Ser Ser  
185 190 195



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	CTG CCA GCT AGA AAA CCA CCA AAT GAA CCC CAT GTT TAC TTG CCC GGT	677
	Leu Pro Ala Arg Lys Pro Pro Asn Glu Pro His Val Tyr Leu Pro Gly	
	200 205 210	
5	TTA ATA ATT CTG CTT CTC TTC GCG TCT GTG GCC CTG GTG GCT GCC ATC	725
	Leu Ile Ile Leu Leu Leu Phe Ala Ser Val Ala Leu Val Ala Ala Ile	
	215 220 225	
10	ATC TTT GGC GTT TGC TAT AGG AAA AAA GGG AAA GCA CTC ACA GCT AAT	773
	Ile Phe Gly Val Cys Tyr Arg Lys Lys Gly Lys Ala Leu Thr Ala Asn	
	230 235 240 245	
15	TTG TGG CAC TGG ATC AAT GAG GCT TGT GGC CGC CTA AGT GGA GAT AAG	821
	Leu Trp His Trp Ile Asn Glu Ala Cys Gly Arg Leu Ser Gly Asp Lys	
	250 255 260	
20	GAG TCC TCA GGT GAC AGT TGT GTC AGT ACA CAC ACG GCA AAC TTT GGT	869
	Glu Ser Ser Gly Asp Ser Cys Val Ser Thr His Thr Ala Asn Phe Gly	
	265 270 275	
25	CAG CAG GGA GCA TGT GAA GGT GTC TTA CTG CTG ACT CTG GAG GAG AAG	917
	Gln Gln Gly Ala Cys Glu Gly Val Leu Leu Leu Thr Leu Glu Glu Lys	
	280 285 290	
	ACA TTT CCA GAA GAT ATG TGC TAC CCA GAT CAA GGT GGT GTC TGT CAG	965
	Thr Phe Pro Glu Asp Met Cys Tyr Pro Asp Gln Gly Gly Val Cys Gln	
	295 300 305	
30	GGC ACG TGT GTA GGA GGT GGT CCC TAC GCA CAA GGC GAA GAT GCC AGG	1013
	Gly Thr Cys Val Gly Gly Gly Pro Tyr Ala Gln Gly Glu Asp Ala Arg	
	310 315 320 325	
35	ATG CTC TCA TTG GTC AGC AAG ACC GAG ATA GAG GAA GAC AGC TTC AGA	1061
	Met Leu Ser Leu Val Ser Lys Thr Glu Ile Glu Glu Asp Ser Phe Arg	
	330 335 340	
40	CAG ATG CCC ACA GAA GAT GAA TAC ATG GAC AGG CCC TCC CAG CCC ACA	1109
	Gln Met Pro Thr Glu Asp Glu Tyr Met Asp Arg Pro Ser Gln Pro Thr	
	345 350 355	
45	GAC CAG TTA CTG TTC CTC ACT GAG CCT GGA AGC AAA TCC ACA CCT CCT	1157
	Asp Gln Leu Leu Phe Leu Thr Glu Pro Gly Ser Lys Ser Thr Pro Pro	
	360 365 370	
	TTC TCT GAA CCC CTG GAG GTG GGG GAG AAT GAC AGT TTA AGC CAG TGC	1205
	Phe Ser Glu Pro Leu Glu Val Gly Glu Asn Asp Ser Leu Ser Gln Cys	
	375 380 385	
50	TTC ACG GGG ACA CAG AGC ACA GTG GGT TCA GAA AGC TGC AAC TGC ACT	1253
	Phe Thr Gly Thr Gln Ser Thr Val Gly Ser Glu Ser Cys Asn Cys Thr	
	390 395 400 405	
55	GAG CCC CTG TGC AGG ACT GAT TGG ACT CCC ATG TCC TCT GAA AAC TAC	1301
	Glu Pro Leu Cys Arg Thr Asp Trp Thr Pro Met Ser Ser Glu Asn Tyr	
	410 415 420	
60	TTG CAA AAA GAG GTG GAC AGT GGC CAT TGC CCG CAC TGG GCA GCC AGC	1349
	Leu Gln Lys Glu Val Asp Ser Gly His Cys Pro His Trp Ala Ala Ser	
	425 430 435	

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CCC AGC CCC AAC TGG GCA GAT GTC TGC ACA GGC TGC CGG AAC  
Pro Ser Pro Asn Trp Ala Asp Val Cys Thr Gly Cys Arg Asn  
440 445 450

1391

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 451 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Pro Arg Ala Arg Arg Arg Arg Pro Leu Phe Ala Leu Leu Leu  
1 5 10 15  
Leu Cys Ala Leu Leu Ala Arg Leu Gln Val Ala Leu Gln Ile Ala Pro  
20 25 30  
Pro Cys Thr Ser Glu Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn  
35 40 45  
Lys Cys Glu Pro Gly Lys Tyr Met Ser Ser Lys Cys Thr Thr Thr Ser  
50 55 60  
Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp  
65 70 75 80  
Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys  
85 90 95  
Ala Leu Val Ala Val Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys  
100 105 110  
Ala Cys Thr Ala Gly Tyr His Trp Ser Gln Asp Cys Glu Cys Cys Arg  
115 120 125  
Arg Asn Thr Glu Cys Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln  
130 135 140  
Leu Asn Lys Asp Thr Val Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser  
145 150 155 160  
Asp Ala Phe Ser Ser Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr  
165 170 175  
Phe Leu Gly Lys Arg Val Glu His His Gly Thr Glu Lys Ser Asp Ala  
180 185 190  
Val Cys Ser Ser Ser Leu Pro Ala Arg Lys Pro Pro Asn Glu Pro His  
195 200 205  
Val Tyr Leu Pro Gly Leu Ile Ile Leu Leu Leu Phe Ala Ser Val Ala  
210 215 220  
Leu Val Ala Ala Ile Ile Phe Gly Val Cys Tyr Arg Lys Lys Gly Lys  
225 230 235 240

00688459 "101300

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Leu Ser Gly Asp Lys Glu Ser Ser Gly Asp Ser Cys Val Ser Thr His  
5           260                 265                 270

10 Thr Leu Glu Glu Lys Thr Phe Pro Glu Asp Met Cys Tyr Pro Asp Gln  
290 295 300

15 Gly Glu Asp Ala Arg Met Leu Ser Leu Val Ser Lys Thr Glu Ile Glu  
325 330 335

Pro Ser Gln Pro Thr Asp Gln Leu Leu Phe Leu Thr Glu Pro Gly Ser  
355 360 365

25    Lys Ser Thr Pro Pro Phe Ser Glu Pro Leu Glu Val Gly Glu Asn Asp  
               370                          375                          380

30 Ser Cys Asn Cys Thr Glu Pro Leu Cys Arg Thr Asp Trp Thr Pro Met  
405 410 415

35 Ser Ser Glu Asn Tyr Leu Gln Lys Glu Val Asp Ser Gly His Cys Pro  
420 425 430

40 Cys Arg Asn  
450

45 (27) INFORMATION FOR SEQ ID NO:5:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3136 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 50 (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: HOMO SAPIENS

47

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(A) LIBRARY: BONE-MARROW DERIVED DENDRITIC CELLS  
(B) CLONE: FULL LENGTH RANK

## (ix) FEATURE:

5

(A) NAME/KEY: CDS  
(B) LOCATION: 39..1886

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

10

CCGCTGAGGC CGCGGCGCCC GCCAGCCTGT CCCGCGCC ATG GCC CCG CGC GCC 53  
Met Ala Pro Arg Ala  
1 5

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CGG CGG CGC CGC CCG CTG TTC GCG CTG CTG CTG CTC TGC GCG CTG CTC 101  
Arg Arg Arg Arg Pro Leu Phe Ala Leu Leu Leu Leu Cys Ala Leu Leu  
10 15 20

20

GCC CGG CTG CAG GTG GCT TTG CAG ATC GCT CCT CCA TGT ACC AGT GAG 149  
Ala Arg Leu Gln Val Ala Leu Gln Ile Ala Pro Pro Cys Thr Ser Glu  
25 30 35

25

AAG CAT TAT GAG CAT CTG GGA CGG TGC TGT AAC AAA TGT GAA CCA GGA 197  
Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn Lys Cys Glu Pro Gly  
40 45 50

30

AAG TAC ATG TCT TCT AAA TGC ACT ACT ACC TCT GAC AGT GTA TGT CTG 245  
Lys Tyr Met Ser Ser Lys Cys Thr Thr Thr Ser Asp Ser Val Cys Leu  
55 60 65

35

CCC TGT GGC CCG GAT GAA TAC TTG GAT AGC TGG AAT GAA GAA GAT AAA 293  
Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp Asn Glu Glu Asp Lys  
70 75 80 85

40

TGC TTG CTG CAT AAA GTT TGT GAT ACA GGC AAG GCC CTG GTG GCC GTG 341  
Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys Ala Leu Val Ala Val  
90 95 100

45

GTC GCC GGC AAC AGC ACG ACC CCC CGG CGC TGC GCG TGC ACG GCT GGG 389  
Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys Ala Cys Thr Ala Gly  
105 110 115

50

TAC CAC TGG AGC CAG GAC TGC GAG TGC TGC CGC CGC AAC ACC GAG TGC 437  
Tyr His Trp Ser Gln Asp Cys Glu Cys Cys Arg Arg Asn Thr Glu Cys  
120 125 130

GCG CCG GGC CTG GGC GCC CAG CAC CCG TTG CAG CTC AAC AAG GAC ACA 485  
Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln Leu Asn Lys Asp Thr  
135 140 145

GTG TGC AAA CCT TGC CTT GCA GGC TAC TTC TCT GAT GCC TTT TCC TCC 533  
Val Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser Asp Ala Phe Ser Ser  
150 155 160 165

55

ACG GAC AAA TGC AGA CCC TGG ACC AAC TGT ACC TTC CTT GGA AAG AGA 581  
Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr Phe Leu Gly Lys Arg  
170 175 180

60

GTA GAA CAT CAT GGG ACA GAG AAA TCC GAT GCG GTT TGC AGT TCT TCT 629  
Val Glu His His Gly Thr Glu Lys Ser Asp Ala Val Cys Ser Ser Ser  
185 190 195

DDETFOT " 55488999

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5	CTG CCA GCT AGA AAA CCA CCA AAT GAA CCC CAT GTT TAC TTG CCC GGT	677
	Leu Pro Ala Arg Lys Pro Pro Asn Glu Pro His Val Tyr Leu Pro Gly	
	200 205 210	
10	TTA ATA ATT CTG CTT CTC TTC GCG TCT GTG GCC CTG GTG GCT GCC ATC	725
	Leu Ile Ile Leu Leu Leu Phe Ala Ser Val Ala Leu Val Ala Ala Ile	
	215 220 225	
15	ATC TTT GGC GTT TGC TAT AGG AAA AAA GGG AAA GCA CTC ACA GCT AAT	773
	Ile Phe Gly Val Cys Tyr Arg Lys Lys Gly Lys Ala Leu Thr Ala Asn	
	230 235 240 245	
20	TTG TGG CAC TGG ATC AAT GAG GCT TGT GGC CGC CTA AGT GGA GAT AAG	821
	Leu Trp His Trp Ile Asn Glu Ala Cys Gly Arg Leu Ser Gly Asp Lys	
	250 255 260	
25	GAG TCC TCA GGT GAC AGT TGT GTC AGT ACA CAC ACG GCA AAC TTT GGT	869
	Glu Ser Ser Gly Asp Ser Cys Val Ser Thr His Thr Ala Asn Phe Gly	
	265 270 275	
30	CAG CAG GGA GCA TGT GAA GGT GTC TTA CTG CTG ACT CTG GAG GAG AAG	917
	Gln Gln Gly Ala Cys Glu Gly Val Leu Leu Leu Thr Leu Glu Glu Lys	
	280 285 290	
35	ACA TTT CCA GAA GAT ATG TGC TAC CCA GAT CAA GGT GGT GTC TGT CAG	965
	Thr Phe Pro Glu Asp Met Cys Tyr Pro Asp Gln Gly Gly Val Cys Gln	
	295 300 305	
40	GGC ACG TGT GTA GGA GGT GGT CCC TAC GCA CAA GGC GAA GAT GCC AGG	1013
	Gly Thr Cys Val Gly Gly Gly Pro Tyr Ala Gln Gly Glu Asp Ala Arg	
	310 315 320 325	
45	ATG CTC TCA TTG GTC AGC AAG ACC GAG ATA GAG GAA GAC AGC TTC AGA	1061
	Met Leu Ser Leu Val Ser Lys Thr Glu Ile Glu Glu Asp Ser Phe Arg	
	330 335 340	
50	CAG ATG CCC ACA GAA GAT GAA TAC ATG GAC AGG CCC TCC CAG CCC ACA	1109
	Gln Met Pro Thr Glu Asp Glu Tyr Met Asp Arg Pro Ser Gln Pro Thr	
	345 350 355	
55	GAC CAG TTA CTG TTC CTC ACT GAG CCT GGA AGC AAA TCC ACA CCT CCT	1157
	Asp Gln Leu Leu Phe Leu Thr Glu Pro Gly Ser Lys Ser Thr Pro Pro	
	360 365 370	
60	TTC TCT GAA CCC CTG GAG GTG GGG GAG AAT GAC AGT TTA AGC CAG TGC	1205
	Phe Ser Glu Pro Leu Glu Val Gly Glu Asn Asp Ser Leu Ser Gln Cys	
	375 380 385	
65	TTC ACG GGG ACA CAG AGC ACA GTG GGT TCA GAA AGC TGC AAC TGC ACT	1253
	Phe Thr Gly Thr Gln Ser Thr Val Gly Ser Glu Ser Cys Asn Cys Thr	
	390 395 400 405	
70	GAG CCC CTG TGC AGG ACT GAT TGG ACT CCC ATG TCC TCT GAA AAC TAC	1301
	Glu Pro Leu Cys Arg Thr Asp Trp Thr Pro Met Ser Ser Glu Asn Tyr	
	410 415 420	
75	TTG CAA AAA GAG GTG GAC AGT GGC CAT TGC CCG CAC TGG GCA GCC AGC	1349
	Leu Gln Lys Glu Val Asp Ser Gly His Cys Pro His Trp Ala Ala Ser	
	425 430 435	

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TTCTTTTTTT GGCAACCTGG CTCTGGCCCA GGCTAGAGTG CAGTGGTGCG ATTATAGCCC 2406  
 5 GGTGCAGCCT CTAACCTCTG GGCTCAAGCA ATCCAAGTGA TCCTCCCACC TCAACCTTCG 2466  
 GAGTAGCTGG GATCACAGCT GCAGGCCACG CCCAGCTTCC TCCCCCGAC TCCCCCCCCC 2526  
 CAGAGACACG GTCCCACCAT GTTACCCAGC CTGGTCTCAA ACTCCCCAGC TAAAGCAGTC 2586  
 10 CTCCAGCCTC GGCCTCCCAA AGTACTGGGA TTACAGGCGT GAGCCCCCAC GCTGGCCTGC 2646  
 TTTACGTATT TTCTTTTGTG CCCCTGCTCA CAGTGTTTTA GAGATGGCTT TCCCAGTGTG 2706  
 TGTTCATTGT AAACACTTTT GGGAAAGGGC TAAACATGTG AGGCCTGGAG ATAGTTGCTA 2766  
 15 AGTTGCTAGG AACATGTGGT GGGACTTTCA TATTCTGAAA AATGTTCTAT ATTCTCATTT 2826  
 TTCTAAAAGA AAGAAAAAAG GAAACCCGAT TTATTTCTCC TGAATCTTTT TAAGTTTGTG 2886  
 20 TCGTTCCTTA AGCAGAACTA AGCTCAGTAT GTGACCTTAC CCGCTAGGTG GTTAATTTAT 2946  
 CCATGCTGGC AGAGGCACTC AGGTAAGTGG TAAGCAAATT TCTAAAACTC CAAGTTGCTG 3006  
 25 CAGCTTGGCA TTCTTCTTAT TCTAGAGGTC TCTCTGGAAA AGATGGAGAA AATGAACAGG 3066  
 ACATGGGGCT CCTGGAAAGA AAGGGCCCGG GAAGTTCAAG GAAGAATAAA GTTGAAATTT 3126  
 TAAAAAATAA 3136

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 616 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Pro Arg Ala Arg Arg Arg Arg Pro Leu Phe Ala Leu Leu Leu  
 1 5 10 15  
 45 Leu Cys Ala Leu Leu Ala Arg Leu Gln Val Ala Leu Gln Ile Ala Pro  
 20 25 30  
 Pro Cys Thr Ser Glu Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn  
 35 40 45  
 50 Lys Cys Glu Pro Gly Lys Tyr Met Ser Ser Lys Cys Thr Thr Thr Ser  
 50 55 60  
 55 Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp  
 65 70 75 80  
 Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys  
 85 90 95  
 60 Ala Leu Val Ala Val Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys  
 100 105 110

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Ala Cys Thr Ala Gly Tyr His Trp Ser Gln Asp Cys Glu Cys Cys Arg  
115 120 125

5 Arg Asn Thr Glu Cys Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln  
130 135 140

Leu Asn Lys Asp Thr Val Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser  
145 150 155 160

10 Asp Ala Phe Ser Ser Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr  
165 170 175

15 Phe Leu Gly Lys Arg Val Glu His His Gly Thr Glu Lys Ser Asp Ala  
180 185 190

Val Cys Ser Ser Ser Leu Pro Ala Arg Lys Pro Pro Asn Glu Pro His  
195 200 205

20 Val Tyr Leu Pro Gly Leu Ile Ile Leu Leu Leu Phe Ala Ser Val Ala  
210 215 220

Leu Val Ala Ala Ile Ile Phe Gly Val Cys Tyr Arg Lys Lys Gly Lys  
225 230 235 240

25 Ala Leu Thr Ala Asn Leu Trp His Trp Ile Asn Glu Ala Cys Gly Arg  
245 250 255

30 Leu Ser Gly Asp Lys Glu Ser Ser Gly Asp Ser Cys Val Ser Thr His  
260 265 270

Thr Ala Asn Phe Gly Gln Gln Gly Ala Cys Glu Gly Val Leu Leu Leu  
275 280 285

35 Thr Leu Glu Glu Lys Thr Phe Pro Glu Asp Met Cys Tyr Pro Asp Gln  
290 295 300

Gly Gly Val Cys Gln Gly Thr Cys Val Gly Gly Gly Pro Tyr Ala Gln  
305 310 315 320

40 Gly Glu Asp Ala Arg Met Leu Ser Leu Val Ser Lys Thr Glu Ile Glu  
325 330 335

45 Glu Asp Ser Phe Arg Gln Met Pro Thr Glu Asp Glu Tyr Met Asp Arg  
340 345 350

Pro Ser Gln Pro Thr Asp Gln Leu Leu Phe Leu Thr Glu Pro Gly Ser  
355 360 365

50 Lys Ser Thr Pro Pro Phe Ser Glu Pro Leu Glu Val Gly Glu Asn Asp  
370 375 380

Ser Leu Ser Gln Cys Phe Thr Gly Thr Gln Ser Thr Val Gly Ser Glu  
385 390 395 400

55 Ser Cys Asn Cys Thr Glu Pro Leu Cys Arg Thr Asp Trp Thr Pro Met  
405 410 415

60 Ser Ser Glu Asn Tyr Leu Gln Lys Glu Val Asp Ser Gly His Cys Pro  
420 425 430

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His Trp Ala Ala Ser Pro Ser Pro Asn Trp Ala Asp Val Cys Thr Gly  
 435 440 445

5 Cys Arg Asn Pro Pro Gly Glu Asp Cys Glu Pro Leu Val Gly Ser Pro  
 450 455 460

Lys Arg Gly Pro Leu Pro Gln Cys Ala Tyr Gly Met Gly Leu Pro Pro  
 465 470 475 480

10 Glu Glu Glu Ala Ser Arg Thr Glu Ala Arg Asp Gln Pro Glu Asp Gly  
 485 490 495

Ala Asp Gly Arg Leu Pro Ser Ser Ala Arg Ala Gly Ala Gly Ser Gly  
 500 505 510

15 Ser Ser Pro Gly Gly Gln Ser Pro Ala Ser Gly Asn Val Thr Gly Asn  
 515 520 525

20 Ser Asn Ser Thr Phe Ile Ser Ser Gly Gln Val Met Asn Phe Lys Gly  
 530 535 540

Asp Ile Ile Val Val Tyr Val Ser Gln Thr Ser Gln Glu Gly Ala Ala  
 545 550 555 560

25 Ala Ala Ala Glu Pro Met Gly Arg Pro Val Gln Glu Glu Thr Leu Ala  
 565 570 575

Arg Arg Asp Ser Phe Ala Gly Asn Gly Pro Arg Phe Pro Asp Pro Cys  
 580 585 590

30 Gly Gly Pro Glu Gly Leu Arg Glu Pro Glu Lys Ala Ser Arg Pro Val  
 595 600 605

35 Gln Glu Gln Gly Gly Ala Lys Ala  
 610 615

## (2) INFORMATION FOR SEQ ID NO:7:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 8 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: linear

- 45 (ii) MOLECULE TYPE: peptide

- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: FLAG® peptide

- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asp Tyr Lys Asp Asp Asp Asp Lys  
 1 5

55

## (2) INFORMATION FOR SEQ ID NO:8:

- 60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 232 amino acids  
 (B) TYPE: amino acid

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(D) TOPOLOGY: linear

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(A) ORGANISM: Human

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

15

Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro  
20 25 30

20

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val  
50 55 60

25

30

Asp Trp Leu Asn Gly Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala  
100 105 110

35

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr  
130 135 140

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Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr  
180 185 190

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Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys  
210 215 220

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: CMV (R2780 Leader)

(ix) FEATURE:

- (D) OTHER INFORMATION: Met1-Arg28 is the actual leader peptide; Arg29 strengthens the furin cleavage site; nucleotides encoding Thr30 and Ser31 add a SpeI site.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Ala	Arg	Arg	Leu	Trp	Ile	Leu	Ser	Leu	Leu	Ala	Val	Thr	Leu	Thr
1				5				10						15	
Val	Ala	Leu	Ala	Ala	Pro	Ser	Gln	Lys	Ser	Lys	Arg	Arg	Thr	Ser	
		20						25					30		

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mus musculus

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY:
- (B) CLONE: RANKL

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CC	GGC	GTC	CCA	CAC	GAG	GGT	CCG	CTG	CAC	CCC	GCG	CCT	TCT	GCA	CCG
Gly	Val	Pro	His	Glu	Gly	Pro	Leu	His	Pro	Ala	Pro	Ser	Ala	Pro	
1				5				10						15	

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	GCT	CCG	GCG	CCG	CCA	CCC	GCC	GCC	TCC	CGC	TCC	ATG	TTC	CTG	GCC	CTC	95
	Ala	Pro	Ala	Pro	Pro	Pro	Ala	Ala	Ser	Arg	Ser	Met	Phe	Leu	Ala	Leu	
					20					25					30		
5	CTG	GGG	CTG	GGA	CTG	GGC	CAG	GTG	GTC	TGC	AGC	ATC	GCT	CTG	TTC	CTG	143
	Leu	Gly	Leu	Gly	Leu	Gly	Gln	Val	Val	Cys	Ser	Ile	Ala	Leu	Phe	Leu	
				35				40						45			
10	TAC	TTT	CGA	GCG	CAG	ATG	GAT	CCT	AAC	AGA	ATA	TCA	GAA	GAC	AGC	ACT	191
	Tyr	Phe	Arg	Ala	Gln	Met	Asp	Pro	Asn	Arg	Ile	Ser	Glu	Asp	Ser	Thr	
			50					55					60				
15	CAC	TGC	TTT	TAT	AGA	ATC	CTG	AGA	CTC	CAT	GAA	AAC	GCA	GAT	TTG	CAG	239
	His	Cys	Phe	Tyr	Arg	Ile	Leu	Arg	Leu	His	Glu	Asn	Ala	Asp	Leu	Gln	
		65					70				75						
20	GAC	TCG	ACT	CTG	GAG	AGT	GAA	GAC	ACA	CTA	CCT	GAC	TCC	TGC	AGG	AGG	287
	Asp	Ser	Thr	Leu	Glu	Ser	Glu	Asp	Thr	Leu	Pro	Asp	Ser	Cys	Arg	Arg	
	80					85					90					95	
25	ATG	AAA	CAA	GCC	TTT	CAG	GGG	GCC	GTG	CAG	AAG	GAA	CTG	CAA	CAC	ATT	335
	Met	Lys	Gln	Ala	Phe	Gln	Gly	Ala	Val	Gln	Lys	Glu	Leu	Gln	His	Ile	
				100				105						110			
30	GTG	GGG	CCA	CAG	CGC	TTC	TCA	GGA	GCT	CCA	GCT	ATG	ATG	GAA	GGC	TCA	383
	Val	Gly	Pro	Gln	Arg	Phe	Ser	Gly	Ala	Pro	Ala	Met	Met	Glu	Gly	Ser	
				115				120						125			
35	TGG	TTG	GAT	GTG	GCC	CAG	CGA	GGC	AAG	CCT	GAG	GCC	CAG	CCA	TTT	GCA	431
	Trp	Leu	Asp	Val	Ala	Gln	Arg	Gly	Lys	Pro	Glu	Ala	Gln	Pro	Phe	Ala	
			130					135					140				
40	CAC	CTC	ACC	ATC	AAT	GCT	GCC	AGC	ATC	CCA	TCG	GGT	TCC	CAT	AAA	GTC	479
	His	Leu	Thr	Ile	Asn	Ala	Ala	Ser	Ile	Pro	Ser	Gly	Ser	His	Lys	Val	
		145					150					155					
45	ACT	CTG	TCC	TCT	TGG	TAC	CAC	GAT	CGA	GGC	TGG	GCC	AAG	ATC	TCT	AAC	527
	Thr	Leu	Ser	Ser	Trp	Tyr	His	Asp	Arg	Gly	Trp	Ala	Lys	Ile	Ser	Asn	
	160					165					170					175	
50	ATG	ACG	TTA	AGC	AAC	GGA	AAA	CTA	AGG	GTT	AAC	CAA	GAT	GGC	TTC	TAT	575
	Met	Thr	Leu	Ser	Asn	Gly	Lys	Leu	Arg	Val	Asn	Gln	Asp	Gly	Phe	Tyr	
					180			185							190		
55	TAC	CTG	TAC	GCC	AAC	ATT	TGC	TTT	CGG	CAT	CAT	GAA	ACA	TCG	GGA	AGC	623
	Tyr	Leu	Tyr	Ala	Asn	Ile	Cys	Phe	Arg	His	His	Glu	Thr	Ser	Gly	Ser	
				195				200						205			
60	GTA	CCT	ACA	GAC	TAT	CTT	CAG	CTG	ATG	GTG	TAT	GTC	GTT	AAA	ACC	AGC	671
	Val	Pro	Thr	Asp	Tyr	Leu	Gln	Leu	Met	Val	Tyr	Val	Val	Lys	Thr	Ser	
			210					215					220				
65	ATC	AAA	ATC	CCA	AGT	TCT	CAT	AAC	CTG	ATG	AAA	GGA	GGG	AGC	ACG	AAA	719
	Ile	Lys	Ile	Pro	Ser	Ser	His	Asn	Leu	Met	Lys	Gly	Gly	Ser	Thr	Lys	
		225					230					235					
70	AAC	TGG	TCG	GGC	AAT	TCT	GAA	TTC	CAC	TTT	TAT	TCC	ATA	AAT	GTT	GGG	767
	Asn	Trp	Ser	Gly	Asn	Ser	Glu	Phe	His	Phe	Tyr	Ser	Ile	Asn	Val	Gly	
	240					245					250					255	

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GGA TTT TTC AAG CTC CGA GCT GGT GAA GAA ATT AGC ATT CAG GTG TCC 815  
 Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser  
 260 265 270

5 AAC CCT TCC CTG CTG GAT CCG GAT CAA GAT GCG ACG TAC TTT GGG GCT 863  
 Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala  
 275 280 285

10 TTC AAA GTT CAG GAC ATA GAC TGAGACTCAT TTCGTGGAAC ATTAGCATGG 914  
 Phe Lys Val Gln Asp Ile Asp  
 290

ATGTCCTAGA TGTTTGAAAA CTTCTTAAAA AATGGATGAT GTCTATACAT GTGTAAGACT 974

15 ACTAAGAGAC ATGGCCCACG GTGTATGAAA CTCACAGCCC TCTCTCTTGA GCCTGTACAG 1034  
 GTTGTGTATA TGTAAGTCC ATAGGTGATG TTAGATTCAT GGTGATTACA CAACGGTTTT 1094

20 ACAATTTTGT AATGATTTCC TAGAATTGAA CCAGATTGGG AGAGGTATTC CGATGCTTAT 1154  
 GAAAACTTA CACGTGAGCT ATGGAAGGGG GTCACAGTCT CTGGGTCTAA CCCCTGGACA 1214

TGTGCCACTG AGAACCTTGA AATTAAGAGG ATGCCATGTC ATTGCAAAGA AATGATAGTG 1274

25 TGAAGGGTTA AGTTCTTTTG AATTGTTACA TTGCGCTGGG ACCTGCAAAT AAGTTCTTTT 1334  
 TTTCTAATGA GGAGAGAAAA ATATATGTAT TTTTATATAA TGTCTAAAGT TATATTTTCTAG 1394

30 GTGTAATGTT TTCTGTGCAA AGTTTTGTAA ATTATATTTG TGCTATAGTA TTTGATTCAA 1454  
 AATATTTAAA AATGTCTCAC TGTGACATA TTTAATGTTT TAAATGTACA GATGTATTTA 1514

ACTGGTGCAC TTTGTAATTC CCCTGAAGGT ACTCGTAGCT AAGGGGGCAG AATACTGTTT 1574

35 CTGGTGACCA CATGTAGTTT ATTTCTTTAT TCTTTTAAAC TTAATAGAGT CTTCAG 1630

## (2) INFORMATION FOR SEQ ID NO:11:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 294 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

50 Gly Val Pro His Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala  
 1 5 10 15

Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu  
 20 25 30

55 Gly Leu Gly Leu Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr  
 35 40 45

Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His  
 50 55 60

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Cys Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Asp Leu Gln Asp  
 65 70 75 80  
 5 Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met  
 85 90 95  
 Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val  
 100 105 110  
 10 Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp  
 115 120 125  
 Leu Asp Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His  
 130 135 140  
 15 Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr  
 145 150 155 160  
 20 Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met  
 165 170 175  
 Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr  
 180 185 190  
 25 Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val  
 195 200 205  
 Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile  
 210 215 220  
 30 Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn  
 225 230 235 240  
 35 Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly  
 245 250 255  
 Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn  
 260 265 270  
 40 Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe  
 275 280 285  
 Lys Val Gln Asp Ile Asp  
 290  
 45

(2) INFORMATION FOR SEQ ID NO:12:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 954 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 55 (ii) MOLECULE TYPE: cDNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 60 (vi) ORIGINAL SOURCE:

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(A) ORGANISM: Homo sapiens

## (vii) IMMEDIATE SOURCE:

(A) LIBRARY:

(B) CLONE: huRANKL (full length)

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..951

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

15	ATG CGC CGC GCC AGC AGA GAC TAC ACC AAG TAC CTG CGT GGC TCG GAG Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser Glu	48
	1 5 10 15	
20	GAG ATG GGC GGC GGC CCC GGA GCC CCG CAC GAG GGC CCC CTG CAC GCC Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His Ala	96
	20 25 30	
25	CCG CCG CCG CCT GCG CCG CAC CAG CCC CCC GCC GCC TCC CGC TCC ATG Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser Met	144
	35 40 45	
30	TTC GTG GCC CTC CTG GGG CTG GGG CTG GGC CAG GTT GTC TGC AGC GTC Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Val	192
	50 55 60	
35	GCC CTG TTC TTC TAT TTC AGA GCG CAG ATG GAT CCT AAT AGA ATA TCA Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser	240
	65 70 75 80	
40	GAA GAT GGC ACT CAC TGC ATT TAT AGA ATT TTG AGA CTC CAT GAA AAT Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn	288
	85 90 95	
45	GCA GAT TTT CAA GAC ACA ACT CTG GAG AGT CAA GAT ACA AAA TTA ATA Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile	336
	100 105 110	
50	CCT GAT TCA TGT AGG AGA ATT AAA CAG GCC TTT CAA GGA GCT GTG CAA Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln	384
	115 120 125	
55	AAG GAA TTA CAA CAT ATC GTT GGA TCA CAG CAC ATC AGA GCA GAG AAA Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys	432
	130 135 140	
60	GCG ATG GTG GAT GGC TCA TGG TTA GAT CTG GCC AAG AGG AGC AAG CTT Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu	480
	145 150 155 160	
65	GAA GCT CAG CCT TTT GCT CAT CTC ACT ATT AAT GCC ACC GAC ATC CCA Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro	528
	165 170 175	
70	TCT GGT TCC CAT AAA GTG AGT CTG TCC TCT TGG TAC CAT GAT CGG GGT Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly	576
	180 185 190	

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TGG GCC AAG ATC TCC AAC ATG ACT TTT AGC AAT GGA AAA CTA ATA GTT 624  
 Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val  
 195 200 205

5 AAT CAG GAT GGC TTT TAT TAC CTG TAT GCC AAC ATT TGC TTT CGA CAT 672  
 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His  
 210 215 220

10 CAT GAA ACT TCA GGA GAC CTA GCT ACA GAG TAT CTT CAA CTA ATG GTG 720  
 His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val  
 225 230 235 240

15 TAC GTC ACT AAA ACC AGC ATC AAA ATC CCA AGT TCT CAT ACC CTG ATG 768  
 Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met  
 245 250 255

20 AAA GGA GGA AGC ACC AAG TAT TGG TCA GGG AAT TCT GAA TTC CAT TTT 816  
 Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe  
 260 265 270

25 TAT TCC ATA AAC GTT GGT GGA TTT TTT AAG TTA CGG TCT GGA GAG GAA 864  
 Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu  
 275 280 285

30 ATC AGC ATC GAG GTC TCC AAC CCC TCC TTA CTG GAT CCG GAT CAG GAT 912  
 Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp  
 290 295 300

30 GCA ACA TAC TTT GGG GCT TTT AAA GTT CGA GAT ATA GAT TGA 954  
 Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp  
 305 310 315

35 (2) INFORMATION FOR SEQ ID NO:13:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 317 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

45 Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser Glu  
 1 5 10 15

50 Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His Ala  
 20 25 30

55 Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser Met  
 35 40 45

60 Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Val  
 50 55 60

65 Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser  
 65 70 75 80

60 Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn  
 85 90 95

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Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile  
100 105 110

5 Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln  
115 120 125

Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys  
130 135 140

10 Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu  
145 150 155 160

15 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro  
165 170 175

Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly  
180 185 190

20 Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val  
195 200 205

Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His  
210 215 220

25 His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val  
225 230 235 240

30 Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met  
245 250 255

Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe  
260 265 270

35 Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu  
275 280 285

Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp  
290 295 300

40 Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp  
305 310 315

45

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1878 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- 55 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 60 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Murine

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(ix) FEATURE:

(B) LOCATION: 1..1875

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

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ACC CTC CTT GGA AAG CTA GAA GCA CAC CAG GGG ACA ACG GAA TCA GAT 576  
Thr Leu Leu Gly Lys Leu Glu Ala His Gln Gly Thr Thr Glu Ser Asp  
180 185 190

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	GTG	GTC	TGC	AGC	TCT	TCC	ATG	ACA	CTG	AGG	AGA	CCA	CCC	AAG	GAG	GCC	624
	Val	Val	Cys	Ser	Ser	Ser	Met	Thr	Leu	Arg	Arg	Pro	Pro	Lys	Glu	Ala	
			195					200					205				
5	CAG	GCT	TAC	CTG	CCC	AGT	CTC	ATC	GTT	CTG	CTC	CTC	TTC	ATC	TCT	GTG	672
	Gln	Ala	Tyr	Leu	Pro	Ser	Leu	Ile	Val	Leu	Leu	Leu	Phe	Ile	Ser	Val	
		210					215					220					
10	GTA	GTA	GTG	GCT	GCC	ATC	ATC	TTC	GGC	GTT	TAC	TAC	AGG	AAG	GGA	GGG	720
	Val	Val	Val	Ala	Ala	Ile	Ile	Phe	Gly	Val	Tyr	Tyr	Arg	Lys	Gly	Gly	
		225				230					235					240	
15	AAA	GCG	CTG	ACA	GCT	AAT	TTG	TGG	AAT	TGG	GTC	AAT	GAT	GCT	TGC	AGT	768
	Lys	Ala	Leu	Thr	Ala	Asn	Leu	Trp	Asn	Trp	Val	Asn	Asp	Ala	Cys	Ser	
				245						250					255		
20	AGT	CTA	AGT	GGA	AAT	AAG	GAG	TCC	TCA	GGG	GAC	CGT	TGT	GCT	GGT	TCC	816
	Ser	Leu	Ser	Gly	Asn	Lys	Glu	Ser	Ser	Gly	Asp	Arg	Cys	Ala	Gly	Ser	
				260						265					270		
25	CAC	TCG	GCA	ACC	TCC	AGT	CAG	CAA	GAA	GTG	TGT	GAA	GGT	ATC	TTA	CTA	864
	His	Ser	Ala	Thr	Ser	Ser	Gln	Gln	Glu	Val	Cys	Glu	Gly	Ile	Leu	Leu	
			275					280					285				
30	ATG	ACT	CGG	GAG	GAG	AAG	ATG	GTT	CCA	GAA	GAC	GGT	GCT	GGA	GTC	TGT	912
	Met	Thr	Arg	Glu	Glu	Lys	Met	Val	Pro	Glu	Asp	Gly	Ala	Gly	Val	Cys	
		290					295					300					
35	GGG	CCT	GTG	TGT	GCG	GCA	GGT	GGG	CCC	TGG	GCA	GAA	GTC	AGA	GAT	TCT	960
	Gly	Pro	Val	Cys	Ala	Ala	Gly	Gly	Pro	Trp	Ala	Glu	Val	Arg	Asp	Ser	
		305				310					315					320	
40	AGG	ACG	TTC	ACA	CTG	GTC	AGC	GAG	GTT	GAG	ACG	CAA	GGA	GAC	CTC	TCG	1008
	Arg	Thr	Phe	Thr	Leu	Val	Ser	Glu	Val	Glu	Thr	Gln	Gly	Asp	Leu	Ser	
				325						330					335		
45	AGG	AAG	ATT	CCC	ACA	GAG	GAT	GAG	TAC	ACG	GAC	CGG	CCC	TCG	CAG	CCT	1056
	Arg	Lys	Ile	Pro	Thr	Glu	Asp	Glu	Tyr	Thr	Asp	Arg	Pro	Ser	Gln	Pro	
				340					345					350			
50	TCG	ACT	GGT	TCA	CTG	CTC	CTA	ATC	CAG	CAG	GGA	AGC	AAA	TCT	ATA	CCC	1104
	Ser	Thr	Gly	Ser	Leu	Leu	Leu	Ile	Gln	Gln	Gly	Ser	Lys	Ser	Ile	Pro	
			355					360					365				
55	CCA	TTC	CAG	GAG	CCC	CTG	GAA	GTG	GGG	GAG	AAC	GAC	AGT	TTA	AGC	CAG	1152
	Pro	Phe	Gln	Glu	Pro	Leu	Glu	Val	Gly	Glu	Asn	Asp	Ser	Leu	Ser	Gln	
		370					375					380					
60	TGT	TTC	ACC	GGG	ACT	GAA	AGC	ACG	GTG	GAT	TCT	GAG	GGC	TGT	GAC	TTC	1200
	Cys	Phe	Thr	Gly	Thr	Glu	Ser	Thr	Val	Asp	Ser	Glu	Gly	Cys	Asp	Phe	
		385				390					395					400	
65	ACT	GAG	CCT	CCG	AGC	AGA	ACT	GAC	TCT	ATG	CCC	GTG	TCC	CCT	GAA	AAG	1248
	Thr	Glu	Pro	Pro	Ser	Arg	Thr	Asp	Ser	Met	Pro	Val	Ser	Pro	Glu	Lys	
				405						410					415		
70	CAC	CTG	ACA	AAA	GAA	ATA	GAA	GGT	GAC	AGT	TGC	CTC	CCC	TGG	GTG	GTC	1296
	His	Leu	Thr	Lys	Glu	Ile	Glu	Gly	Asp	Ser	Cys	Leu	Pro	Trp	Val	Val	
				420					425					430			

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AGC TCC AAC TCA ACA GAT GGC TAC ACA GGC AGT GGG AAC ACT CCT GGG 1344  
 Ser Ser Asn Ser Thr Asp Gly Tyr Thr Gly Ser Gly Asn Thr Pro Gly  
           435                                  440                                  445

5 GAG GAC CAT GAA CCC TTT CCA GGG TCC CTG AAA TGT GGA CCA TTG CCC 1392  
 Glu Asp His Glu Pro Phe Pro Gly Ser Leu Lys Cys Gly Pro Leu Pro  
           450                                  455                                  460

10 CAG TGT GCC TAC AGC ATG GGC TTT CCC AGT GAA GCA GCA GCC AGC ATG 1440  
 Gln Cys Ala Tyr Ser Met Gly Phe Pro Ser Glu Ala Ala Ala Ser Met  
           465                                  470                                  475                                  480

15 GCA GAG GCG GGA GTA CGG CCC CAG GAC AGG GCT GAT GAG AGG GGA GCC 1488  
 Ala Glu Ala Gly Val Arg Pro Gln Asp Arg Ala Asp Glu Arg Gly Ala  
                                   485                                  490                                  495

20 TCA GGG TCC GGG AGC TCC CCC AGT GAC CAG CCA CCT GCC TCT GGG AAC 1536  
 Ser Gly Ser Gly Ser Ser Pro Ser Asp Gln Pro Pro Ala Ser Gly Asn  
                                   500                                  505                                  510

25 GTG ACT GGA AAC AGT AAC TCC ACG TTC ATC TCT AGC GGG CAG GTG ATG 1584  
 Val Thr Gly Asn Ser Asn Ser Thr Phe Ile Ser Ser Gly Gln Val Met  
           515                                  520                                  525

30 AAC TTC AAG GGT GAC ATC ATC GTG GTG TAT GTC AGC CAG ACC TCG CAG 1632  
 Asn Phe Lys Gly Asp Ile Ile Val Val Tyr Val Ser Gln Thr Ser Gln  
           530                                  535                                  540

35 GAG GGC CCG GGT TCC GCA GAG CCC GAG TCG GAG CCC GTG GGC CGC CCT 1680  
 Glu Gly Pro Gly Ser Ala Glu Pro Glu Ser Glu Pro Val Gly Arg Pro  
           545                                  550                                  555                                  560

40 GTG CAG GAG GAG ACG CTG GCA CAC AGA GAC TCC TTT GCG GGC ACC GCG 1728  
 Val Gln Glu Glu Thr Leu Ala His Arg Asp Ser Phe Ala Gly Thr Ala  
                                   565                                  570                                  575

45 CCG CGC TTC CCC GAC GTC TGT GCC ACC GGG GCT GGG CTG CAG GAG CAG 1776  
 Pro Arg Phe Pro Asp Val Cys Ala Thr Gly Ala Gly Leu Gln Glu Gln  
                                   580                                  585                                  590

50 GGG GCA CCC CGG CAG AAG GAC GGG ACA TCG CGG CCG GTG CAG GAG CAG 1824  
 Gly Ala Pro Arg Gln Lys Asp Gly Thr Ser Arg Pro Val Gln Glu Gln  
           595                                  600                                  605

55 GGT GGG GCG CAG ACT TCA CTC CAT ACC CAG GGG TCC GGA CAA TGT GCA 1872  
 Gly Gly Ala Gln Thr Ser Leu His Thr Gln Gly Ser Gly Gln Cys Ala  
           610                                  615                                  620

60 GAA TGA  
 Glu  
 625

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 625 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

5 Met Ala Pro Arg Ala Arg Arg Arg Arg Gln Leu Pro Ala Pro Leu Leu  
     1                    5                    10                    15  
 Ala Leu Cys Val Leu Leu Val Pro Leu Gln Val Thr Leu Gln Val Thr  
                     20                    25                    30  
 10 Pro Pro Cys Thr Gln Glu Arg His Tyr Glu His Leu Gly Arg Cys Cys  
                     35                    40                    45  
 Ser Arg Cys Glu Pro Gly Lys Tyr Leu Ser Ser Lys Cys Thr Pro Thr  
                     50                    55                    60  
 15 Ser Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Thr  
                     65                    70                    75                    80  
 20 Trp Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Ala Gly  
                     85                    90                    95  
 Lys Ala Leu Val Ala Val Asp Pro Gly Asn His Thr Ala Pro Arg Arg  
                     100                    105                    110  
 25 Cys Ala Cys Thr Ala Gly Tyr His Trp Asn Ser Asp Cys Glu Cys Cys  
                     115                    120                    125  
 Arg Arg Asn Thr Glu Cys Ala Pro Gly Phe Gly Ala Gln His Pro Leu  
                     130                    135                    140  
 30 Gln Leu Asn Lys Asp Thr Val Cys Thr Pro Cys Leu Leu Gly Phe Phe  
                     145                    150                    155                    160  
 35 Ser Asp Val Phe Ser Ser Thr Asp Lys Cys Lys Pro Trp Thr Asn Cys  
                     165                    170                    175  
 Thr Leu Leu Gly Lys Leu Glu Ala His Gln Gly Thr Thr Glu Ser Asp  
                     180                    185                    190  
 40 Val Val Cys Ser Ser Ser Met Thr Leu Arg Arg Pro Pro Lys Glu Ala  
                     195                    200                    205  
 Gln Ala Tyr Leu Pro Ser Leu Ile Val Leu Leu Leu Phe Ile Ser Val  
                     210                    215                    220  
 45 Val Val Val Ala Ala Ile Ile Phe Gly Val Tyr Tyr Arg Lys Gly Gly  
                     225                    230                    235                    240  
 50 Lys Ala Leu Thr Ala Asn Leu Trp Asn Trp Val Asn Asp Ala Cys Ser  
                     245                    250                    255  
 Ser Leu Ser Gly Asn Lys Glu Ser Ser Gly Asp Arg Cys Ala Gly Ser  
                     260                    265                    270  
 55 His Ser Ala Thr Ser Ser Gln Gln Glu Val Cys Glu Gly Ile Leu Leu  
                     275                    280                    285  
 60 Met Thr Arg Glu Glu Lys Met Val Pro Glu Asp Gly Ala Gly Val Cys  
                     290                    295                    300

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Gly Pro Val Cys Ala Ala Gly Gly Pro Trp Ala Glu Val Arg Asp Ser  
 305 310 315 320

5 Arg Thr Phe Thr Leu Val Ser Glu Val Glu Thr Gln Gly Asp Leu Ser  
 325 330 335

Arg Lys Ile Pro Thr Glu Asp Glu Tyr Thr Asp Arg Pro Ser Gln Pro  
 340 345 350

10 Ser Thr Gly Ser Leu Leu Leu Ile Gln Gln Gly Ser Lys Ser Ile Pro  
 355 360 365

Pro Phe Gln Glu Pro Leu Glu Val Gly Glu Asn Asp Ser Leu Ser Gln  
 370 375 380

15 Cys Phe Thr Gly Thr Glu Ser Thr Val Asp Ser Glu Gly Cys Asp Phe  
 385 390 395 400

Thr Glu Pro Pro Ser Arg Thr Asp Ser Met Pro Val Ser Pro Glu Lys  
 405 410 415

His Leu Thr Lys Glu Ile Glu Gly Asp Ser Cys Leu Pro Trp Val Val  
 420 425 430

25 Ser Ser Asn Ser Thr Asp Gly Tyr Thr Gly Ser Gly Asn Thr Pro Gly  
 435 440 445

Glu Asp His Glu Pro Phe Pro Gly Ser Leu Lys Cys Gly Pro Leu Pro  
 450 455 460

30 Gln Cys Ala Tyr Ser Met Gly Phe Pro Ser Glu Ala Ala Ala Ser Met  
 465 470 475 480

35 Ala Glu Ala Gly Val Arg Pro Gln Asp Arg Ala Asp Glu Arg Gly Ala  
 485 490 495

Ser Gly Ser Gly Ser Ser Pro Ser Asp Gln Pro Pro Ala Ser Gly Asn  
 500 505 510

40 Val Thr Gly Asn Ser Asn Ser Thr Phe Ile Ser Ser Gly Gln Val Met  
 515 520 525

Asn Phe Lys Gly Asp Ile Ile Val Val Tyr Val Ser Gln Thr Ser Gln  
 530 535 540

45 Glu Gly Pro Gly Ser Ala Glu Pro Glu Ser Glu Pro Val Gly Arg Pro  
 545 550 555 560

50 Val Gln Glu Glu Thr Leu Ala His Arg Asp Ser Phe Ala Gly Thr Ala  
 565 570 575

Pro Arg Phe Pro Asp Val Cys Ala Thr Gly Ala Gly Leu Gln Glu Gln  
 580 585 590

55 Gly Ala Pro Arg Gln Lys Asp Gly Thr Ser Arg Pro Val Gln Glu Gln  
 595 600 605

60 Gly Gly Ala Gln Thr Ser Leu His Thr Gln Gly Ser Gly Gln Cys Ala  
 610 615 620

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Glu  
625

5 (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro  
 1 5 10 15

20 Gly Ser Thr Gly  
 20

25 (2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 5 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

35 Asp Tyr Lys Asp Glu  
 5

40 (2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

50 His His His His His His  
 5

55 (2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

60

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

5    Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile  
      1                               5                               10                               15  
     Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu  
                              20                               25                               30  
10    Arg

15

09683459-101300  
DOCTO" 6548960